Supplementary Information

Section 1: Methodological aspects of the study

Processing of microclimate data

We quantified particle size of the soil clastic sediment for one sample per plot (n = 50) using a Malvern Mastersizer 3000, which was used to calibrate soil moisture values. Soil texture within all plots was classified as silt loam or silt according to the United States Department of Agriculture[17] (Supplementary Fig. 10) and specified as "silt loam" in the equation to convert raw soil moisture count into volumetric soil water (m^3/m^3) content using the *mc_calc_vwc* function from the myClim package[2].

Duplicated time series were automatically removed by the myClim package. Periods of time when the dataloggers were out of the ground due to wildlife were automatically detected using the *mc_prep_TMSoffsoil* function based on surface temperature measurements with support from field observations to accurately remove data from these periods for all sensors. Visual inspections also showed anomalous spikes in the soil moisture sensor of some loggers, which were identified and removed. The resultant data gaps were replaced with imputed data based on the mean of other loggers in the plot at the same time point resulting in 2.78% and 1.33% of soil moisture and temperature being imputed respectively (Supplementary Fig. 11 and 12).

Processing of soil nutrient samples

Soil cores were taken at all six replicates per plot using an auger of 42.5 mm to a depth of 10 cm (n = 300). Once in the lab, soil was passed through a 4 mm sieve to homogenise the soil and remove any roots, stones, and leaves. 5 g +/- 0.05 of soil was weighed and the exact mass recorded. 25 ml of 1 M KCl Milli-Q® solution was dispensed into each sample tube. The samples were left to shake for 1-hr at 200 rpm and subsequently centrifuged for 5-mins at 2900 g. Once centrifuged, the solution of each sample was poured into a syringe with a filter inside and samples transferred into a new sample tube. A Shimadzu TOC-L CPH, with a TNM-L total nitrogen module, with high salinity settings and catalyst type was used. The furnace was set to 720°C and zero air carrier gas used at a rate of 150 ml per min. Samples were pretreated with 2% 9 N H2SO4 acid and sparged for 90-secs with 100 ml per min of zero air to remove any potential carbonate or bicarbonate prior to injection of 150 µL of the sample on the combustion tube. The instrument was calibrated before each set of country analyses.

Processing of soil pH samples

Soil cores were taken at five stations per plot using an auger of 25.4 mm diameter to a depth of 10 cm in order to directly compare with the soil eDNA (n = 250). pH was measured following a protocol provided by the Food and Agriculture Organization of the United Nations[3]. A precision balance was used to weigh soil to 5 g +/- 0.05 g and 25 ml of 0.05 M calcium chloride solution added to each sample before shaking at 200 rpm for 1-hr at room temperature and samples let to rest for 1-hr. A Fisherbrand™ accumet™ AE150 pH electrode with built-in temperature sensor turned on 15-mins prior to taking measurements to warm up and calibrated using buffers traceable to NIST Standard Reference Material. The probe was held in the $CaCl_2$ solution just above the settled soil until the value settled which was recorded. The probe was cleaned between each sample with DI water.

Extraction of eDNA from soil

In the field, soil samples were stored in sterile Whirl-Paks® (United States) and the auger cleaned with ethanol between replicates. Samples were kept refrigerated for one week, before being transported on ice to the lab at the University of Bristol for freezer storage before being freeze-dried. To extract the soil eDNA, 250 mg +/- 0.05 of soil was weighed from each sample, 1 ml of SL1 and 50 µL of SX were added to the soil and placed on a vortex to shake for 30-mins. Samples were then centrifuged at 17,000 rpm for 4-mins and the supernatant transferred to a new tube before repeating this step with 2-mins on the centrifuge. Next, 150 µL of SL3 was added and the samples vortexed for 5-secs before being incubated on ice for 5-mins and centrifuged for 1-min. Avoiding the pellet, the supernatant was loaded into a red spin column with a filter and centrifuged for 1-min keeping the flow through. In the binding step, 250 µL was added to the spin column and vortexed for 5-secs before being loaded onto the green spin column with a filter in batches 550 µL at a time. Each time the samples were centrifuged for 1-min and the flow through discarded. In the washing step, 500 µL of SB, 550 µL of SW1, 650 µL of 70% ethanol, 650 µL of SW2, and a second round of 650 µL of SW2 were passed through the filter and allowed to incubate for 3-mins before centrifuging after each wash for 1-min and discarding the flow through each time. Once washing was complete, samples were dried in a centrifuge for 2-mins twice. Finally 50 µL of SE elution buffer was added and allowed to incubate for 1-min with the lid open before centrifuging for 1-min. Samples were stored frozen and transferred on dry ice to BGI for metabarcoding using 16S, 18S, and ITS2 primers.

PCR conditions

In the first amplification step, PCRs were carried out in reagent containing 21 µL of ultrapure water and 30 ng of template DNA, 25 µL of 2x Phanta Max Master Mix (Vazyme. P515), 2 µL 10 µM forward primer, and 2 µL 10 µM reverse primer. The reaction mixture was incubated as follows: an initial denaturation at 95°C for 3-mins, 95°C for 30-secs, an annealing step of 35 cycles at 95°C for 45-secs, 72°C for 45-secs, and a final extension step at 72°C for 10-mins.

Bioinformatics processing of barcodes using Metaworks

Amplicon sequence variants (ASVs) were identified for all barcodes using the MetaWorks v1.13.0 workflow[4]. SeqPrep v1.3.2 was used for merging of read pairs[5] and Cutadapt v4.1 for primer- and quality-trimming[6]. MetaWorks employed VSEARCH v2.21.1[7] for generating denoised, chimera-filtered ASVs. Only ASVs with at least eight reads were retained. The ITS2x program trimmed away the flanking conserved rRNA gene sequences from the ITS2 sequences to improve taxonomic assignments[8]. The reads were mapped to the ASVs with the *search_exact* command of VSEARCH.

Structure of generalised linear mixed effects models (GLMMs)

Model 1: Relative contribution of within- and between-site factors to decay rates

R code: *glmmTMB(formula = decomp_rate ~ 1 + (1 | site:plot), ziformula = ~1, data = model_data, family = ziGamma(link = "log"), control = glmmTMBControl(optimizer = optim, optArgs = list(method = "BFGS")))*

Equation:

$$
\begin{gathered}
0 \sim Bernoulli(\xi)\ if\ y_i = 0 \\
y_i \sim (1 - \xi) \cdot Gamma\left(\alpha, \frac{\alpha}{\mu_i}\right)\ if\ y_i \neq 0 \\
\mu_i = exp\ (\beta_0 + u_{plot[i].country[i]}) \\
u_{plot,country} \sim Normal\big(0, \sigma_{plot,country}\big)
\end{gathered}
$$

Model 2: Hierarchical partitioning of biotic and abiotic factors associated with decay rates

R code: *glmmTMB(formula = decomp_rate ~ site + bag_treat + substrate + conifer_proportion + pH + total_nitrogen + mean_daily_temp + mean_daily_moist + pcoa1_16s + pcoa1_18s + pcoa1_its + pcoa2_16s + pcoa2_18s + pcoa2_its + (1|plot), ziformula = ~1, data = model_data_no_NAs, family = ziGamma(link = "log"), control = glmmTMBControl(optimizer = optim, optArgs = list(method = "BFGS")))*

Equation:

$$0 \sim Bernoulli(\xi)\ if\ y_i = 0$$

$$y_i \sim (1 - \xi) \cdot Gamma\left(\alpha, \frac{\alpha}{\mu_i}\right)\ if\ y_i \neq 0$$

$$
\begin{aligned}
\mu_i = exp\ (\beta_0 + \beta_{country[i]} + \beta_{bag\_treatment[i]} + \beta_{substrate[i]} + \ \beta_1 \cdot conifer_i + \beta_2 \cdot pH_i + \beta_3 \\
\cdot total_{N_i} + \beta_4 \cdot temperature_i + \beta_5 \cdot moisture_i + \beta_6 \cdot PCoA1\colon 16S_i + \beta_7 \\
\cdot PCoA2\colon 16S_i + \beta_8 \cdot PCoA1\colon 18S_i + \beta_9 \cdot PCoA2\colon 18S_i + \beta_{10} \cdot PCoA1\colon ITS_i + \beta_{11} \\
\cdot PCoA2\colon ITS_i + u_{plot[i]})
\end{aligned}
$$

$$u_{plot} \sim Normal\big(0, \sigma_{plot}\big)$$

Model 3: Associations between soil biotic groups and decay rates

R code: *glmmTMB(formula = decomp_rate ~ (PCoA1 + PCoA2) * substrate + (1|site/plot), ziformula = ~1, data = model_data, family = ziGamma(link = "log"), control = glmmTMBControl(optimizer = optim, optArgs = list(method = "BFGS")))*

Equation:

$$0 \sim Bernoulli(\xi)\ if\ y_i = 0$$
$$y_i \sim (1 - \xi) \cdot Gamma\left(\alpha, \frac{\alpha}{\mu_i}\right)\ if\ y_i \neq 0$$
$$\mu_i = exp\ (\beta_0 + \beta_1 \cdot PCoA1_i + \beta_2 \cdot PCoA2_i + \beta_{substrate} + \beta_{substrate2[i]} \cdot PCoA1_i + \beta_{susbtrate3[i]} \cdot PCoA2_i + u_{site[i]} + u_{plot[i].site[i]})$$
$$u_{site} \sim Normal(0, \sigma_{site})$$
$$u_{plot,site} \sim Normal(0, \sigma_{plot,site})$$

Model 4: Associations between microclimatic conditions and decay rates

R code: *glmmTMB(formula = decomp_rate ~ substrate:(temperature + I(temperature ^2)) + substrate + temperature + I(temperature ^2) + (1|site/plot), ziformula = ~1, data = model_data, family = ziGamma(link = "log"), control = glmmTMBControl(optimizer = optim, optArgs = list(method = "BFGS")))*

Equation:

$$0 \sim Bernoulli(\xi)\ if\ y_i = 0$$

$$y_i \sim (1 - \xi) \cdot Gamma\left(\alpha, \frac{\alpha}{\mu_i}\right)\ if\ y_i \neq 0$$

$$\mu_i = exp\ (\beta_0 + \beta_{substrate[i]} + \beta_1 \cdot temperature_i + \beta_2 \cdot temperature_i^2 + \beta_{substrate2[i]} \cdot temperature_i + \beta_{substrate3[i]} \cdot temperature_i^2 + u_{site[i]} + u_{plot[i].site[i]})$$

$$u_{site} \sim Normal(0, \sigma_{site})$$

$$u_{plot,site} \sim Normal(0, \sigma_{plot,site})$$

Where *y* is the response variable at index *i*, ξ is the probability of a measurement being 0, α is the shape parameter, μ is the linear predictor, β are the fixed effects coefficients, and σ the random effect variance for a given site and plot combination. $\beta_{substrate}$, $\beta_{bag\_treatment}$ and β_{site} represent categorical coefficients for each level of substrate, bag treatment and site respectively.

Section 2: Extended results of the study

Drivers of soil biotic community composition

Community composition (determined by Bray-Curtis dissimilarity) of fungi (ITS2) was largely distinct between sites, with the exception of Germany and Finland (Supplementary Fig. 2). Bacterial communities (16S) were less distinct, following a gradient in composition across the sites (Supplementary Fig. 2). Eukaryotic communities including arthropods and worms (hereafter referred to as fauna), protists, and nematodes (18S) (that were considered separately from fauna due to their fundamental role in soil food web dynamics and recycling functions[9–11]) were also largely distinct between sites, with the exception of protists and nematodes in Italy and Romania, which were more similar to one another, indicated by overlapping PCoA clusters (Supplementary Fig. 2). Microclimate temperature, pH, and conifer proportion emerged as the strongest predictors of community composition in all biotic groups (Supplementary Fig. 2; Supplementary Table 6). For example, there was clustering of similar fungal composition in Germany and Finland which was highly correlated with conifer proportion ($R^2 = 0.8$, $P = 0.001$) (Supplementary Fig. 2; Supplementary Table 6). Soil moisture was weakly correlated with community composition across fungi, fauna, protists, and nematodes but no significant relationship with bacterial composition was observed (Supplementary Fig. 2; Supplementary Table 6). Additionally, all community compositions were significantly correlated with total dissolved nitrogen (N) and dissolved organic carbon (DOC) (Supplementary Fig. 2; Supplementary Table 6). Distance-based redundancy analysis revealed environmental variables in the model explained 35-37% of bacterial, 24-26% of fungal, 20-22% of protist, 15-17% of nematode, and 7-10% of faunal community composition.

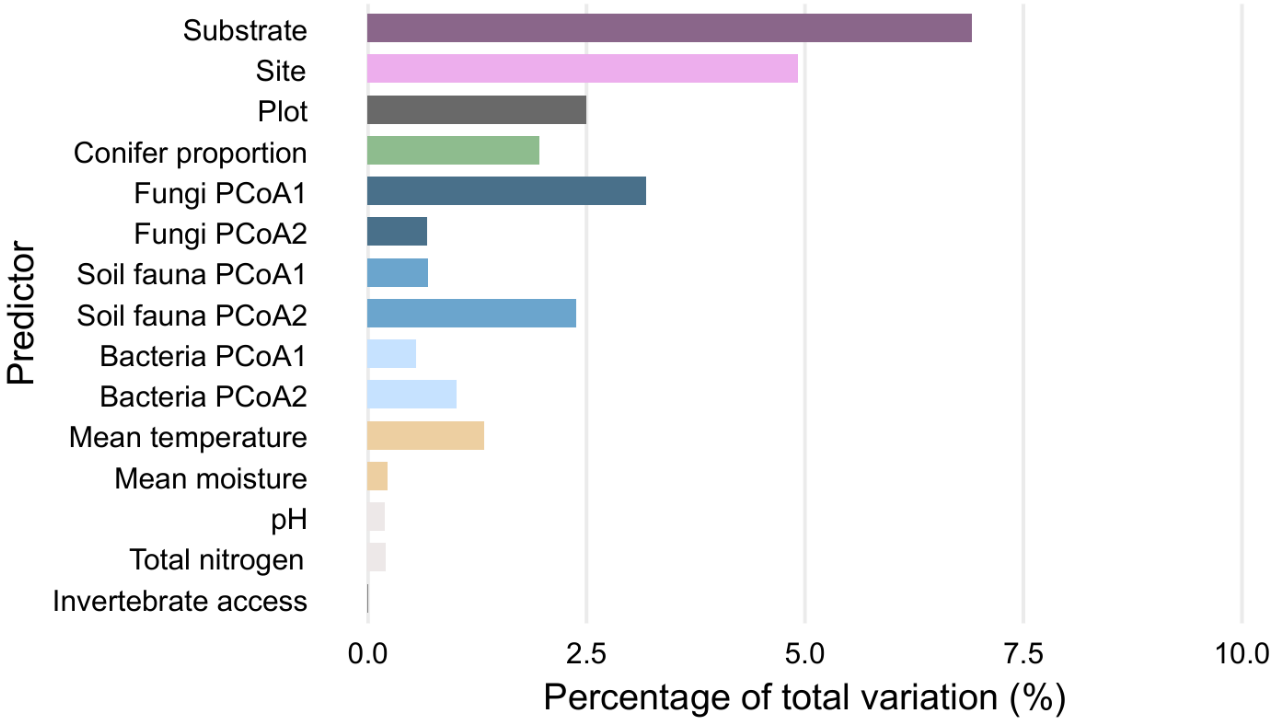
Relative abundance of fungal functional groups and relationships with decay

Across all sites, saprotrophs and ectomycorrhizal (EcM) fungi made up 83.6% of OTUs assigned; 5.9% were wood saprotrophs as their primary lifestyle, 33.1% were soil saprotrophs, 6.5% were litter saprotrophs, and 22.9% were EcM fungi (see Supplementary Fig. 3 for relative proportions of fungal functional groups per site). Wood saprotrophic PCoA1 was positively associated with decomposition rates across substrates ($\beta = 0.209$, $P < 0.001$) (Supplementary Fig. 4; Supplementary Table 9: Model 3). The greatest effect was observed for birch followed by sapele and pine (Supplementary Fig. 4; Supplementary Table 10). We found no relationship between wood saprotrophic PCoA2 and decomposition rates. Total saprotrophic PCoA1 (including taxa capable of decomposing wood, litter, and soil as either their primary or secondary lifestyle) had a positive correlation with decomposition rate ($\beta = 0.213$, $P < 0.001$) which was strongest for birch substrate (Supplementary Fig. 4; Supplementary Tables 9 and 10; Model 3). Total saprotrophic PCoA2 was not correlated with decay ($\beta = 0.0778$, $P = 0.094$) (Supplementary Fig. 4; Supplementary Tables 9; Model 3). Furthermore, we found no relationship between EcM fungal PCoA1 and PCoA2 and decomposition rates (Supplementary Fig. 4; Supplementary Tables 9 and 10; Model 3). There was no association between the species richness of different fungal functional groups and decomposition (Supplementary Fig. 6).

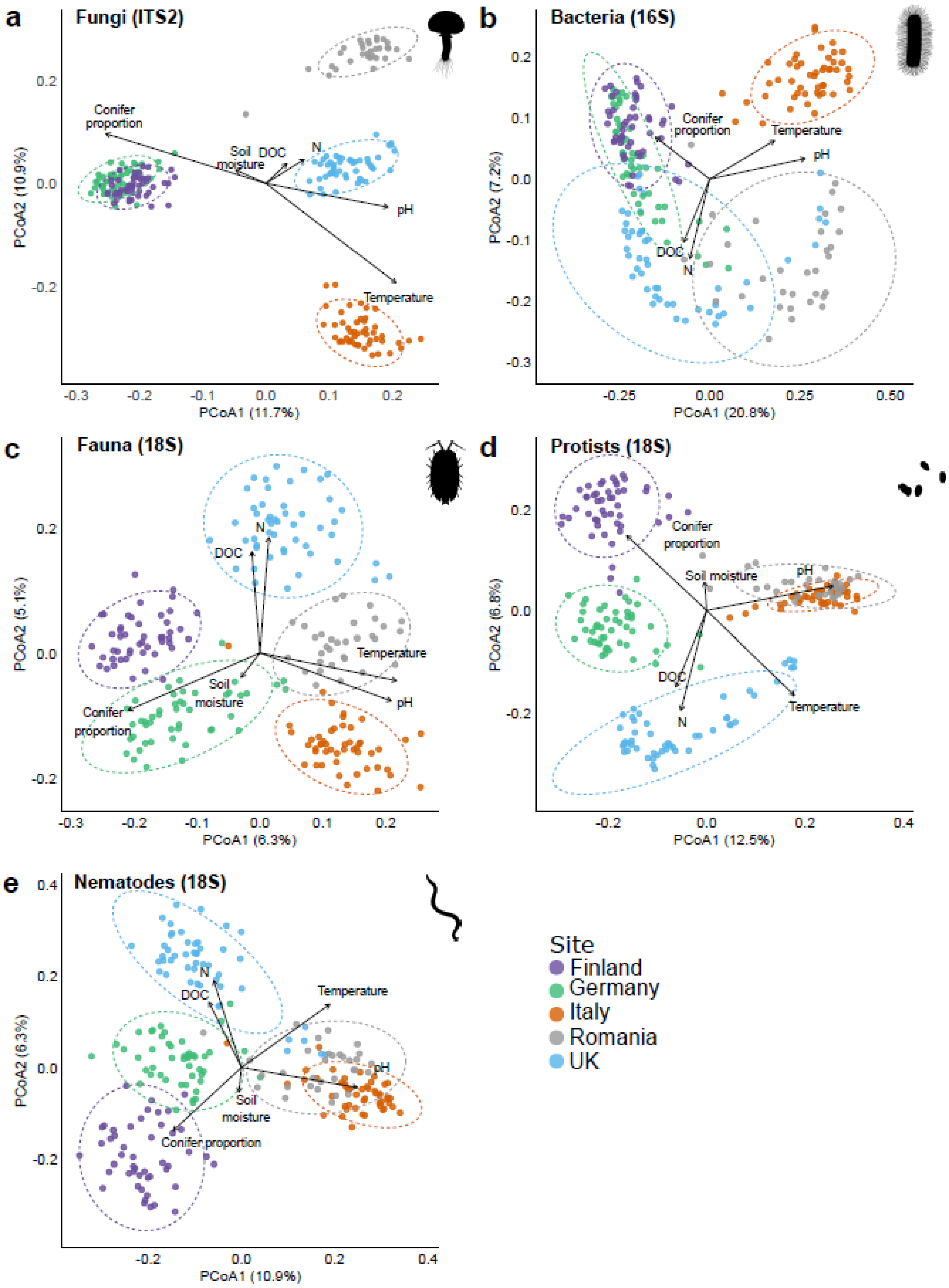
Discussion: Natural wood with bark decomposes more readily than machined wood

Natural birch wood with bark decomposed more rapidly than machined pine and sapele dowel across all sites, with a consistent significant difference observed between birch and sapele. This is despite birch being a hard wood which typically has higher wood density and is slower to decompose than coniferous soft-woods[12,13]. Bark, particularly for hardwood species like birch, may help moderate the microclimate within wood creating an ideal environment for microbial decomposers[12,14]. These results are in agreement with other research demonstrating that natural substrates will yield more representative results in decomposition studies because naturally occurring material is more ecologically relevant, facilitating the colonisation and activity of invertebrates and fungi that would not usually colonise artificial substrates[15,16]. Furthermore, birch was the most temperature and moisture-responsive substrate in our models highlighting the increased effect of decomposer activities in response to environmental conditions for this substrate.

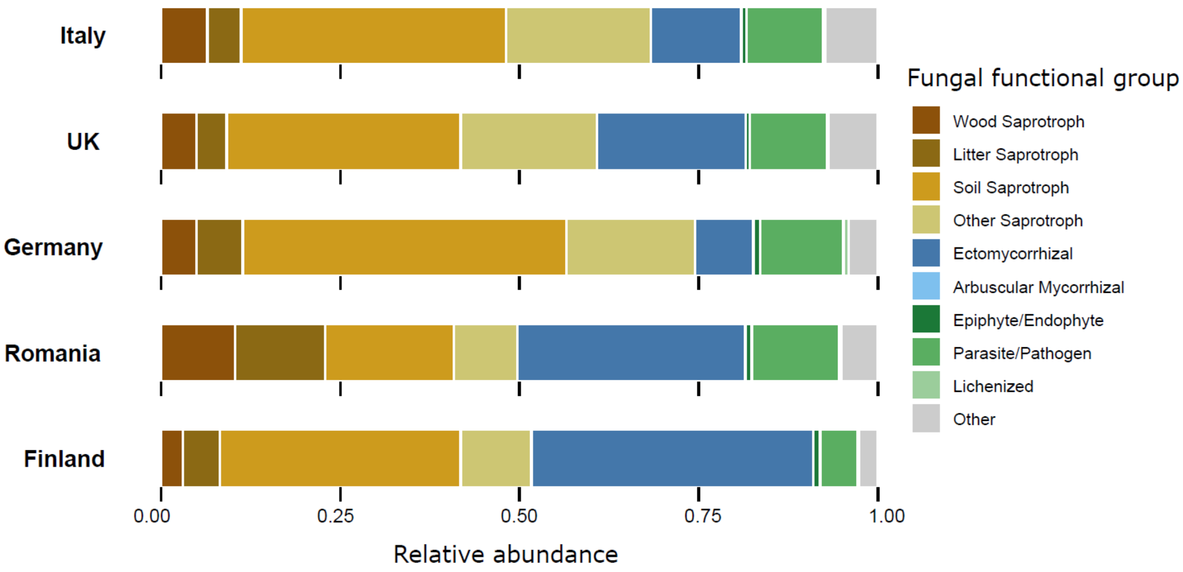
Section 3: Supplementary figures



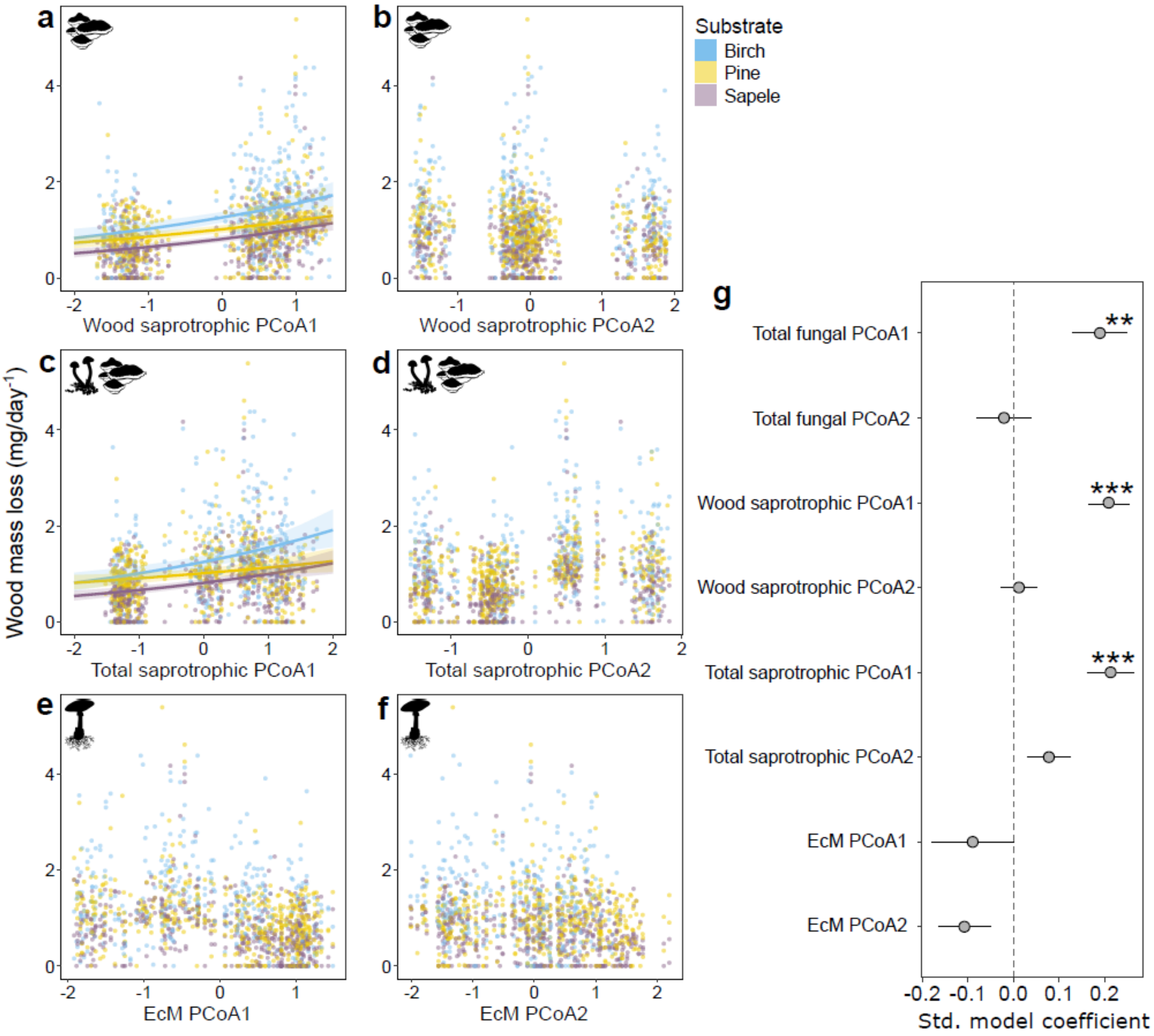
Supplementary Fig. 1: The relative importance of abiotic and biotic factors on deadwood decomposition assessed using hierarchical partitioning. Percentage of total variation represents the combined individual effect of the model predictors including both fixed and random effects (plot) to deadwood decomposition rates. The model explains 28% of variation in decomposition rates total (conditional R^2), 8.9% of which can be attributed to soil community composition, 7.5% to substrate, and 5.2% to site. Continuous predictors were z-transformed for direct comparison.



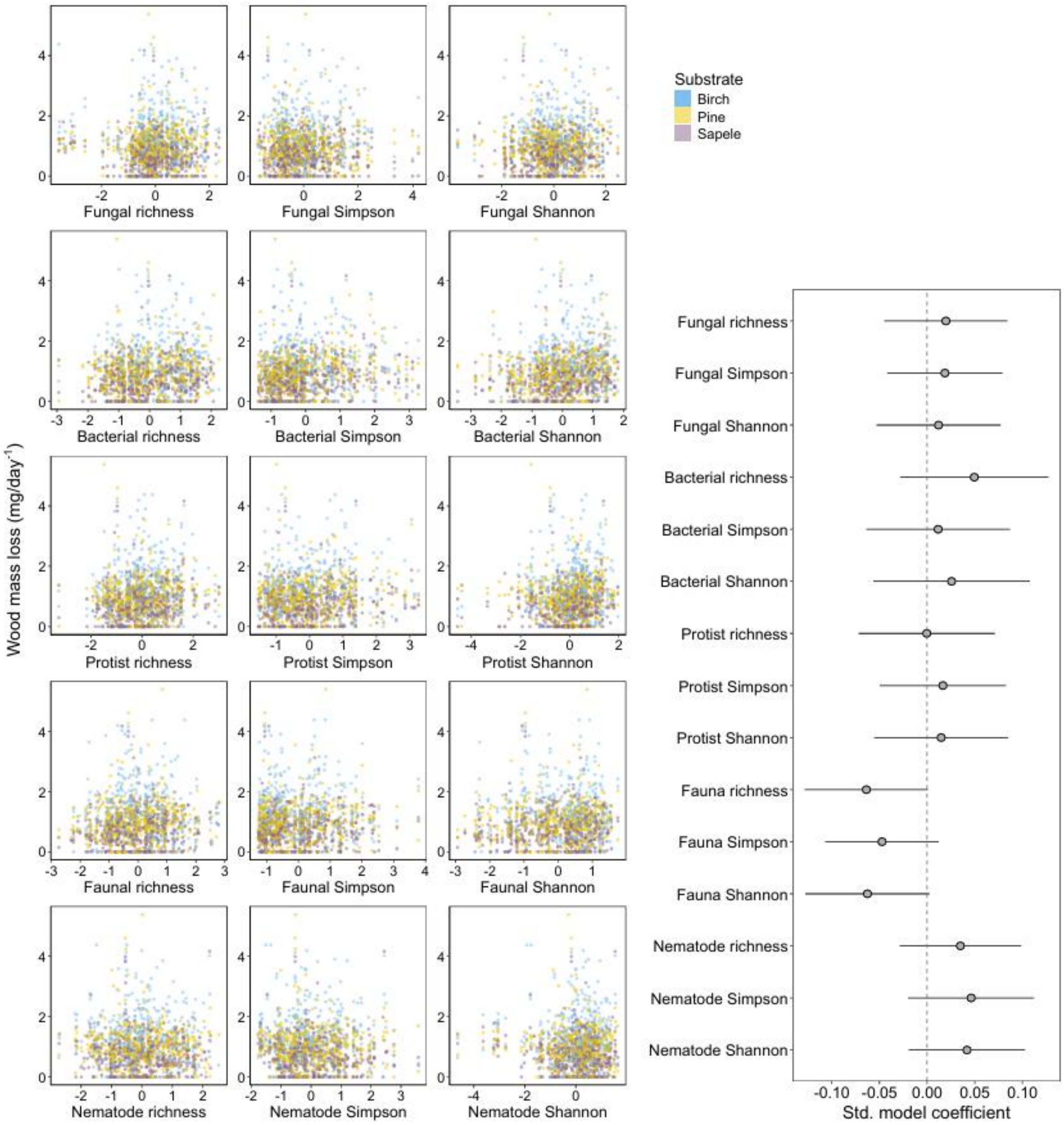
Supplementary Fig 2: Soil fungal (ITS2) **(a)**, bacterial (16S) **(b)**, faunal (18S) **(c)**, protist (18S) **(d)**, and nematode (18S) **(e)** community composition (determined by Bray-Curtis dissimilarity). Fauna (including arthropods and annelids), protists, and nematodes represent 9.3%, 76.9% and 13.8% of 18S ASVs respectively. Axes represent the first two axes of principal coordinates analysis (PCoA) that explain the highest proportion of variance in community composition. Points represent samples taken from the top 10 cm of soil in Finland (purple), Germany (green), Italy (orange), Romania (grey), and UK (blue) for fungi (n = 248), bacteria (n = 249), and fauna, protists and nematodes (n = 245). Vectors (arrows) show significant correlations between z-transformed abiotic factors and the PCoA axes, identified through multiple linear regression in which PCoA axes one and two were predicted by each abiotic variable. Significance of the fitted vectors was tested using 999 permutations of abiotic variables. Abiotic variables include 2 cm air surface temperature (temperature), the proportion of conifer basal area (conifer proportion) in each plot, pH, total dissolved nitrogen (N), dissolved organic carbon (DOC), and volumetric soil water content (soil moisture). Arrow length corresponds to the strength of the correlations. For downstream analyses, protist and bacterial PCoA2 values were multiplied by -1 so that the high end of the axes reflect high soil nitrogen in all ordinations.



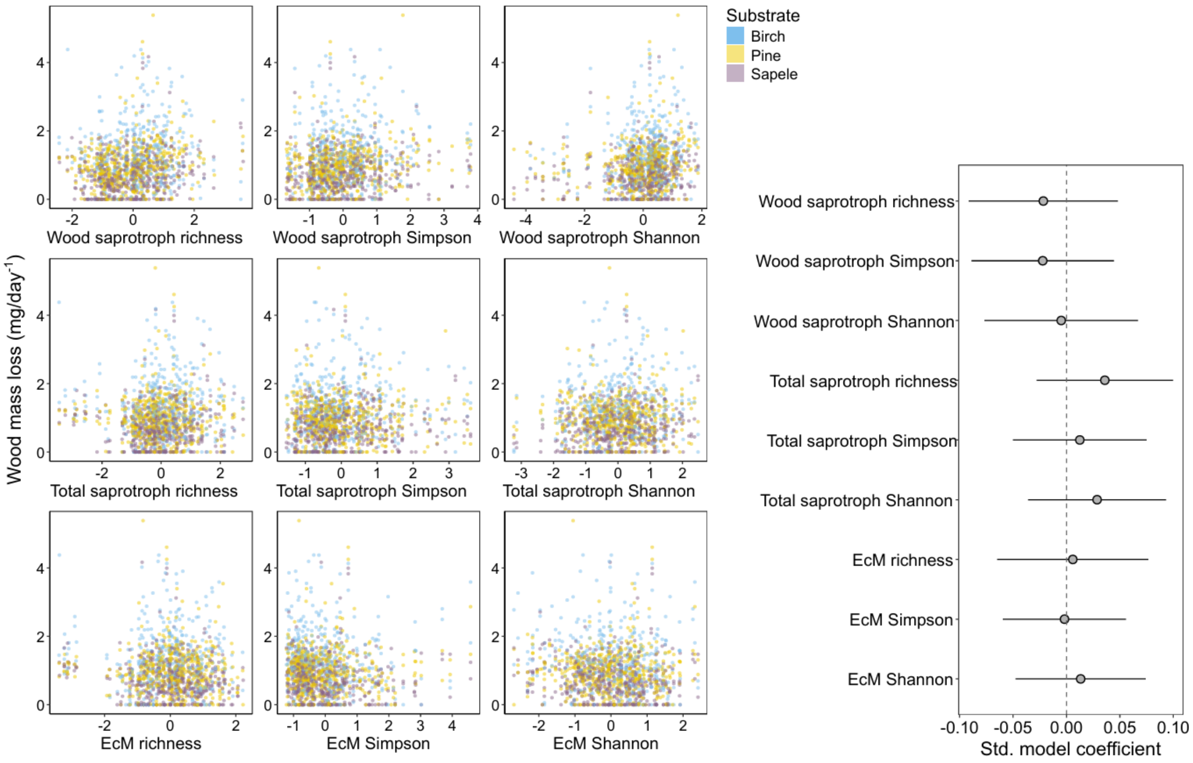
Supplementary Fig. 3: Relative abundance of species assigned to primary functional groups (at the genus level) for Italy, UK, Germany, Romania, and Finland. “Other” represents the relative abundance of species not assigned a function by the FungalTraits database.



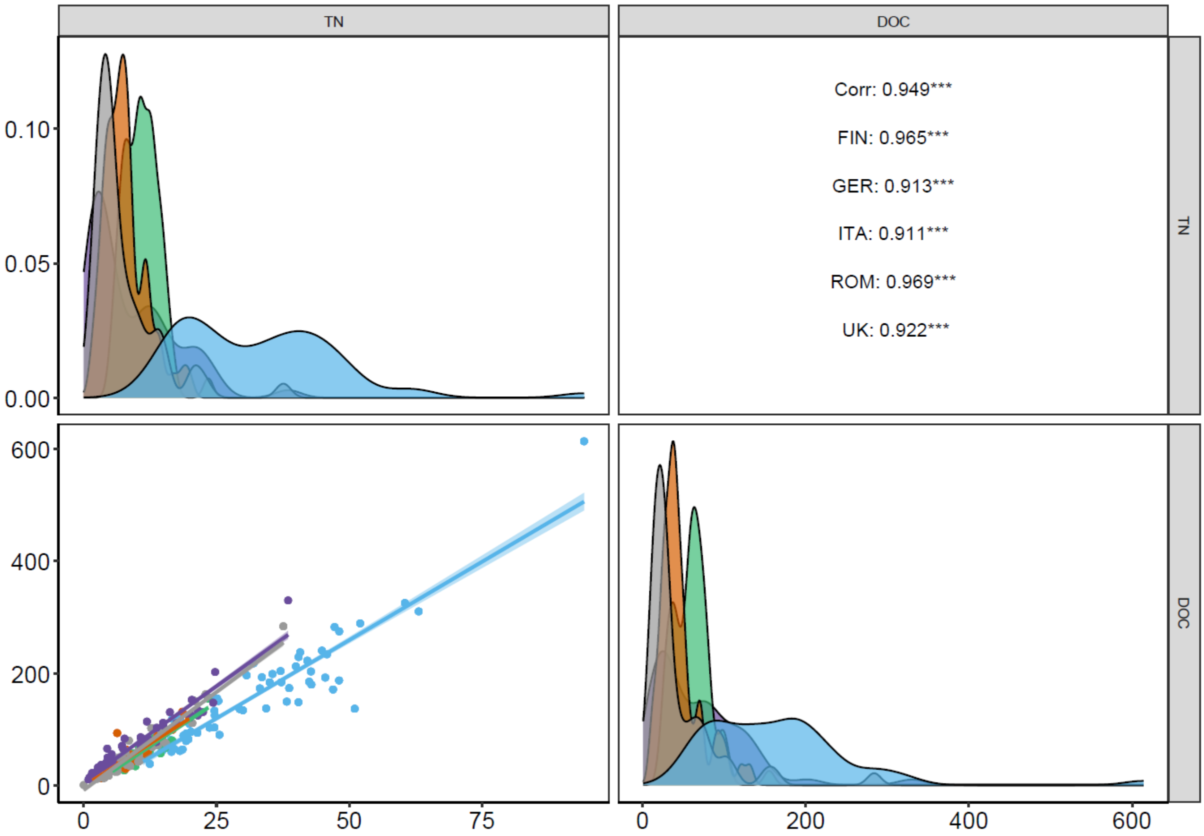
Supplementary Fig. 4: The relationship between wood mass loss (mg/day^{-1}) for three wood types: birch (blue), pine (yellow), and sapele (purple) in response to community composition (PCoA1 and PCoA2) of wood saprotrophs **(a** and **b)**, total saprotrophs (including wood, litter and soil saprotrophs) **(c** and **d)**, and ectomycorrhizal fungi (EcM) **(e** and **f)**. Each soil biodiversity metric has been z-transformed for direct comparison. Ribbons represent the significance of the predicted marginal effects average slope of the interactions between each PCoA axis and substrate with decomposition. Points show the distribution of raw decomposition rates for



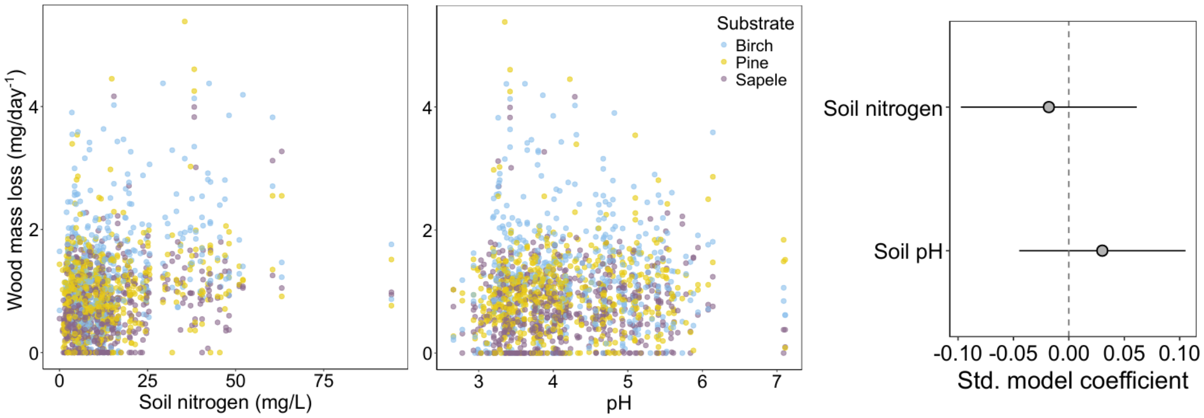
Supplementary Fig. 5: Wood mass loss (mg/day^{-1}) for three wood types: birch (blue), pine (yellow), and sapele (purple) in response to richness, Simpson and Shannon diversity of fungi (ITS2), bacteria (16S), protists (18S), fauna (18S; including arthropods and annelids), and nematodes (18S). Each soil biodiversity metric has been z-transformed for comparison. Points show the distribution of actual decomposition rates for individual wood samples (n = 1,358). Standardised model coefficients for z-transformed soil biology metrics are shown.



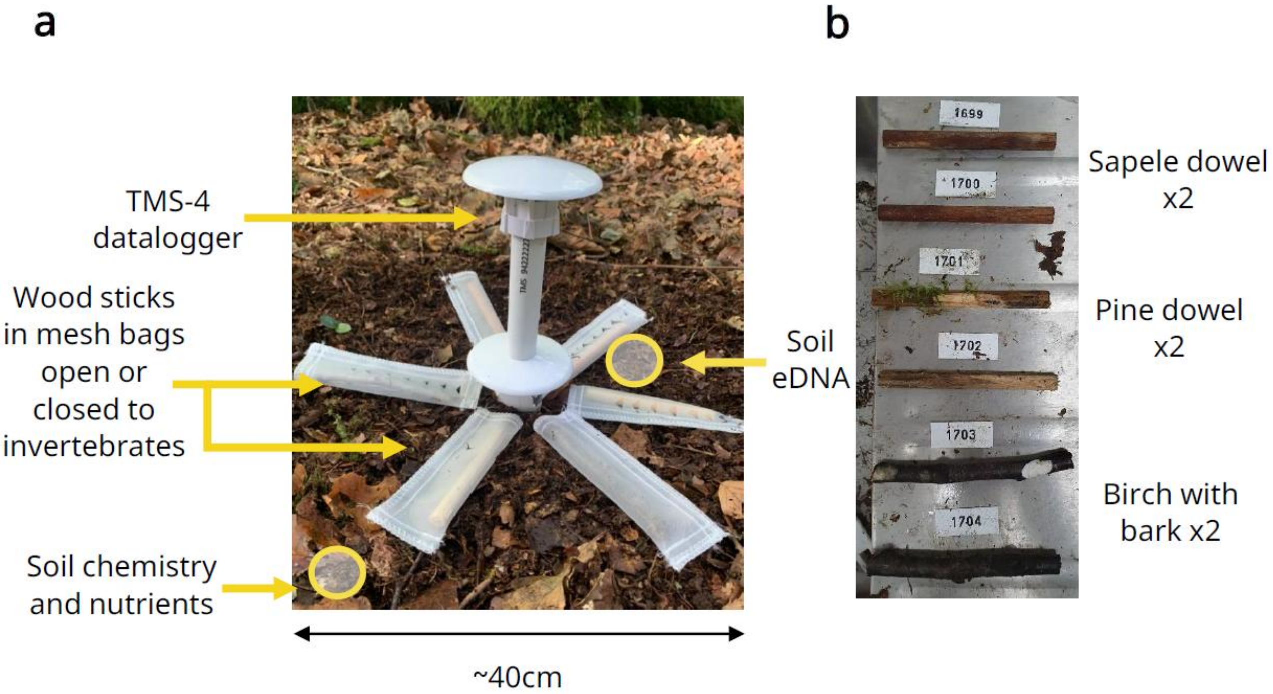
Supplementary Fig. 6: Wood mass loss (mg/day^{-1}) for three wood types: birch (blue), pine (yellow), and sapele (purple) in response to richness, Simpson and Shannon diversity of wood saprotrophs, total saprotrophs (including those capable of decomposing wood, litter, and soil), and ectomycorrhizal fungi (EcM). Each soil biodiversity metric has been z-transformed for comparison. Points show the distribution of actual decomposition rates for individual wood samples (n = 1,358). Standardised model coefficients for z-transformed soil biology metrics are shown.



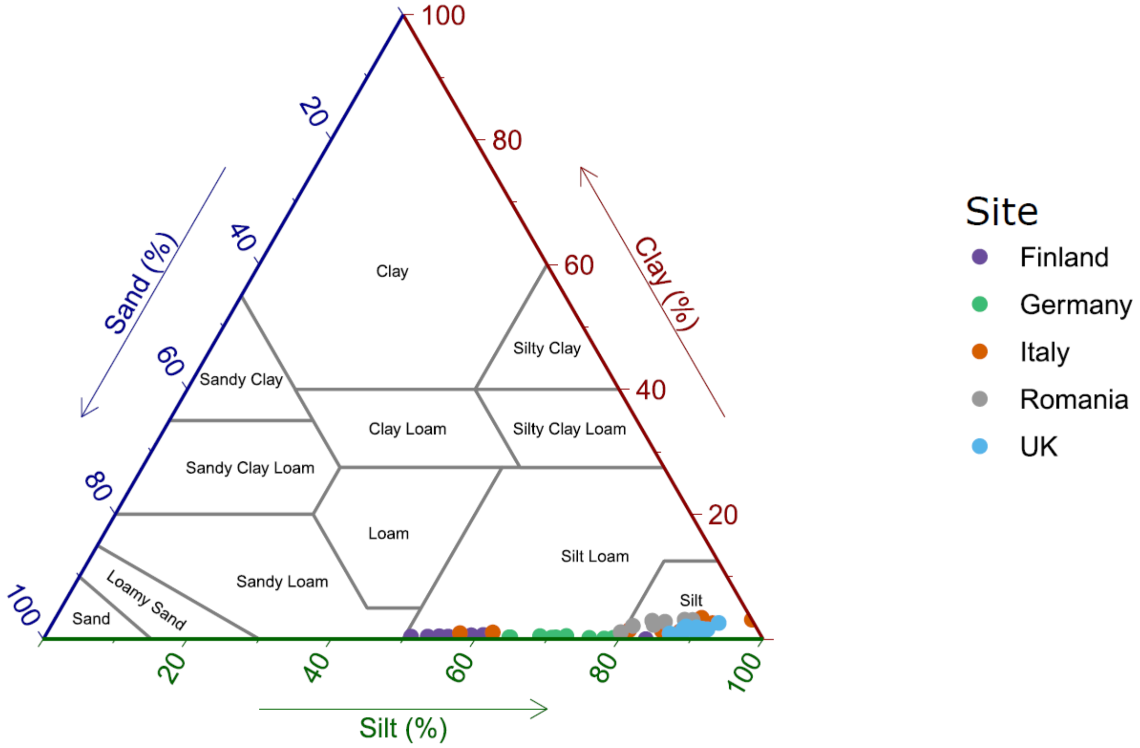
Supplementary Fig. 7: Pairwise relationships between soil nutrient variables across sites. Relationships are shown between total dissolved nitrogen (TN) and dissolved organic carbon (DOC). Points represent individual soil samples, coloured by site: Finland (purple), Germany (green), Italy (orange), Romania (grey), and UK (blue). Bottom left panel displays a scatterplot with linear trend lines. Top right panel displays Pearson correlation coefficients. Top left and bottom right panels represent probability density plots for TN and DOC per site, respectively.



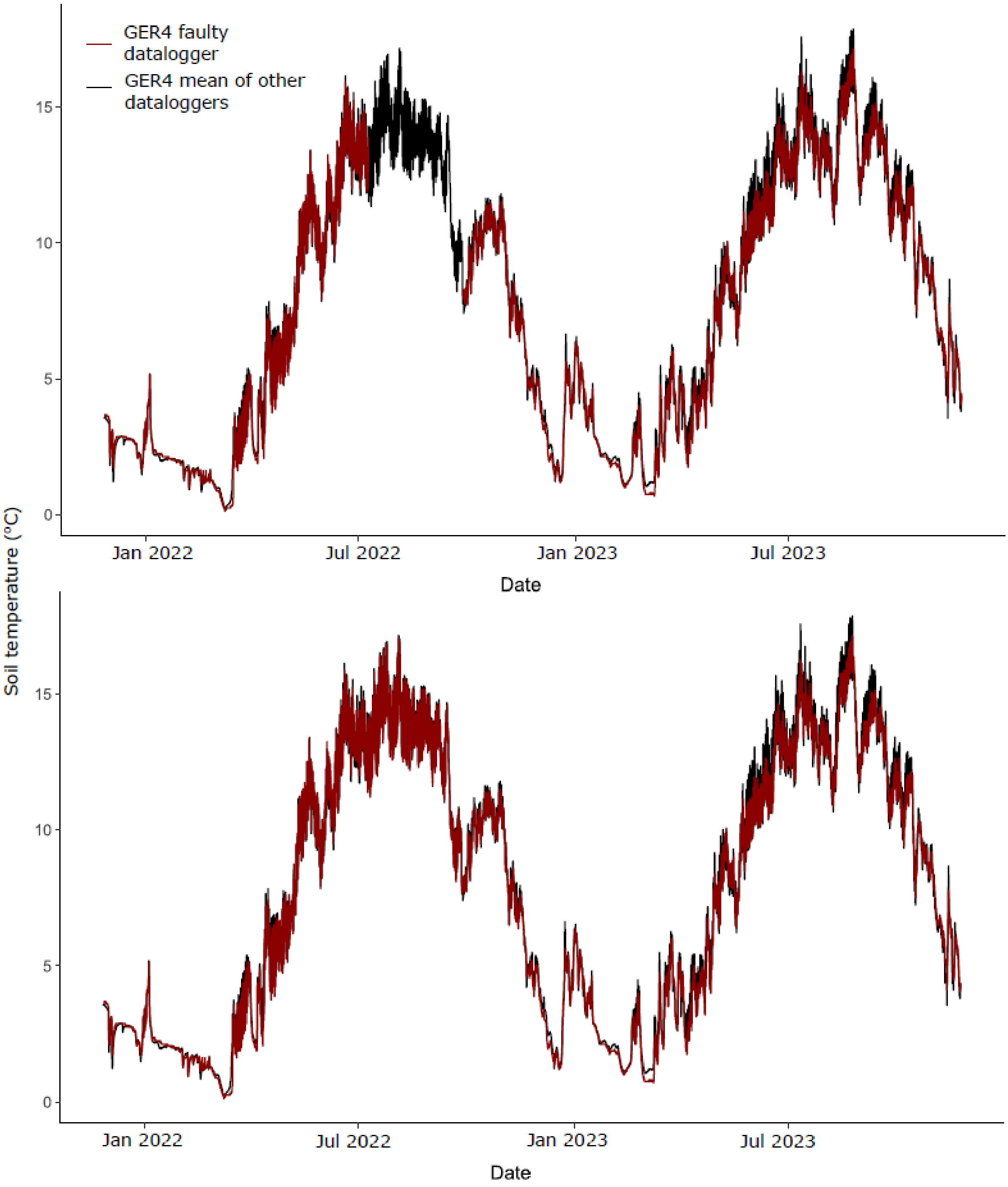
Supplementary Fig. 8: The relationship between wood mass loss (mg/day-1) for three wood types: birch (blue), pine (yellow), and sapele (purple) and soil nitrogen (mg/L) and soil pH. Points show the distribution of raw decomposition rates for individual wood samples (n = 1,632). Standardised model coefficients for z-transformed soil chemistry metrics are shown.



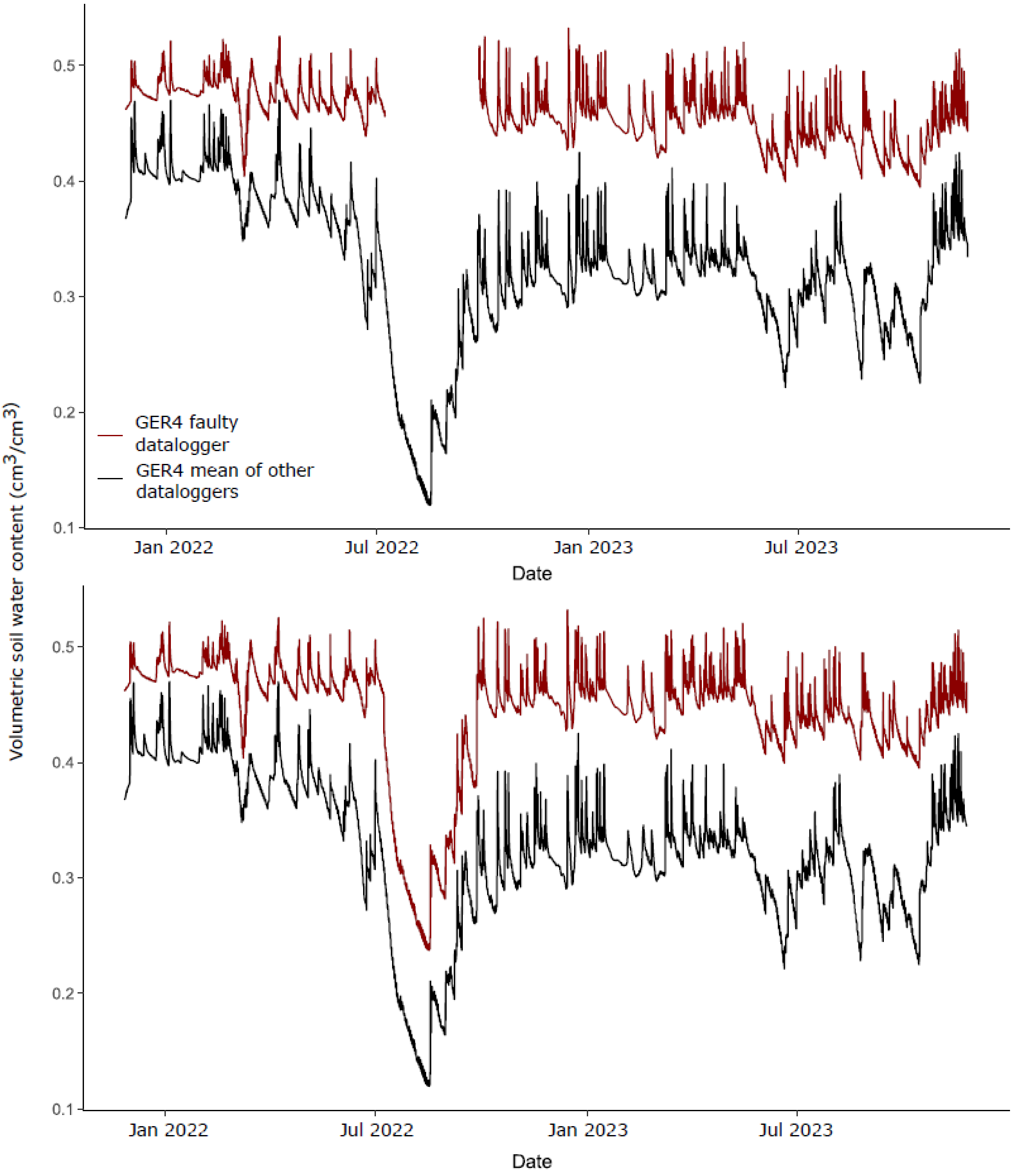
Supplementary Fig. 9: Set-up of the decomposition stations set-up across 50 plots in Europe (n = 300), photo taken in Devon (UK) by Hannah Griffiths **(a)**. TMS-4 datalogger at the centre with a sun hat at the top. The datalogger is surrounded by six wood sticks of three contrasting traits contained within 300 µm diameter mesh bags that were either open to invertebrates (with seven holes cut into the mesh) or closed to invertebrates. Soil eDNA was sampled in close proximity to the wood sticks. Soil pH and nutrients were sampled just outside the wood sticks within ~20 cm of the station. Wood substates used were sapele dowel x 2, pine dowel x 2 and natural birch with bark x 2, photo taken by Emily Bingham **(b)**.



Supplementary Fig. 10: Soil ternary diagram displaying soil classifications. Points represent individual soil samples (one per plot; n = 50) from Finland (purple), Germany (green), Italy (orange), Romania (grey), and the UK (blue). The base triangle is the USDA classification plotted using the ggtern package in R.



Supplementary Fig. 11: Soil temperature over two years for one datalogger (from Germany plot four) which had a three-month period out of the ground (red line) detected by the myClim function *mc_prep_TMSoffsoil* (Man et al. 2023). The mean of the other five dataloggers in the plot with continuous data for the entire time period (black line). The top panel shows the three-month break in the fault datalogger data, whilst the bottom panel shows this period with data imputed from the mean of the other dataloggers offset by the difference between the mean of the faulty datalogger and the combined mean of the other dataloggers for the two year-period.



Supplementary Fig. 12: Volumetric soil water content over two years for one datalogger (from Germany plot four) which had a three-month period out of the ground (red line) detected by the myClim function *mc_prep_TMSoffsoil* (Man et al. 2023). The mean of the other five dataloggers in the plot with continuous data for the entire time period (black line). The top panel shows the three-month break in the faulty datalogger data, whilst the bottom panel shows this period with data imputed from the mean of the other dataloggers offset by the difference between the mean of the faulty datalogger and the combined mean of the other dataloggers for the two-year period.

Section 4: Supplementary tables

Supplementary Table 1: The mean, standard deviation, and coefficient of variation of decomposition rate (mg/day^{-1})) and percentage mass loss of all sticks (n = 1,632) and each substrate separately: birch (n = 464), pine (n = 582), and sapele (n = 586) after two years. Five sites include UK, Romania, Italy, Germany, and Finland, ordered from highest to lowest decay rate. Note that the number of days samples were deployed for varied between sites so percentages cannot be directly compared.

	Mean decomposition rate (mg/day)			
Site	**All substrates**	**Birch**	**Pine**	**Sapele**
UK	1.45 +/- 0.84 (n=358)	1.78 +/- 0.94 (n=119)	1.38 +/- 0.79 (n=119)	1.19 +/- 0.66 (n=120)
Romania	1.1 +/- 0.71 (n=327)	1.34 +/- 0.81 (n=108)	1.14 +/- 0.64 (n=109)	0.82 +/- 0.56 (n=110)
Italy	0.93 +/- 0.63 (n=352)	1.28 +/- 0.67 (n=117)	0.79 +/- 0.54 (n=116)	0.73 +/- 0.51 (n=119)
Germany	0.7 +/- 0.55 (n=359)	0.78 +/- 0.7 (n=120)	0.78 +/- 0.47 (n=119)	0.53 +/- 0.41 (n=120)
Finland	0.59 +/- 0.43 (n=236)	NA	0.74 +/- 0.41 (n=119)	0.43 +/- 0.38 (n=117)

	Mean percentage mass loss (%)			
Site	**All**	**Birch**	**Pine**	**Sapele**
UK	29.41 +/- 16.41	38.99 +/- 16.69	28.62 +/- 15.5	20.69 +/- 11.17
Romania	21.37 +/- 13.04	26.81 +/- 12.81	23.31 +/- 13.02	14.1 +/- 9.67
Italy	16.74 +/- 10.46	22.22 +/- 9.37	15.8 +/- 10.89	12.28 +/- 8.54
Germany	13.5 +/- 10.47	15.24 +/- 12.59	16.14 +/- 9.6	9.13 +/- 7.13
Finland	11.84 +/- 8.89	NA	15.81 +/- 8.82	7.8 +/- 6.96

Supplementary Table 2: Estimated marginal means (EMMs) of daily decomposition rate by site and pairwise comparisons of daily decomposition rates between sites.

glmmTMB(formula = decomp_rate ~ site + (1|plot), ziformula = ~1, data = birch_model_data, family = ziGamma(link = "log"), control = glmmTMBControl(optimizer = optim, optArgs = list(method = "BFGS")))

emmeans(mod, pairwise ~ site, type = "response")

Birch (EMMs)				
Site	**Estimated rate (mg/day)**	**SE**	**Lower 95% CI**	**Upper 95% CI**
Germany	0.848	0.0864	0.695	1.035
Italy	1.298	0.124	1.077	1.565
Romania	1.299	0.126	1.075	1.570
UK	1.8	0.171	1.494	2.170
Birch (Tukey adjusted pairwise comparisons)				
Comparison	**Ratio**	**SE**	**z-ratio**	**p-value**
Germany vs Italy	0.653	0.0912	-3.052	0.0122*
Germany vs Romania	0.653	0.0915	-3.044	0.0125*
Germany vs UK	0.471	0.0656	-5.403	< 0.001***
Italy vs Romania	0.999	0.136	-0.00663	0.999
Italy vs UK	0.721	0.0971	-2.428	0.072
Romania vs UK	0.722	0.0979	-2.406	0.076

Pine (EMMs)				
Site	**Estimated rate (mg/day)**	**SE**	**Lower 95% CI**	**Upper 95% CI**
Germany	0.841	0.0484	0.71	0.89
Italy	0.864	0.0512	0.751	0.941

Romania	1.162	0.0681	0.769	0.97
UK	1.409	0.0802	1.036	1.304
Finland	0.795	0.0458	1.260	1.575
Pine (Tukey adjusted pairwise comparisons)				
Comparison	**Ratio**	**SE**	**z-ratio**	**p-value**
Finland vs Germany	0.946	0.0771	-0.681	0.961
Finland vs Italy	0.921	0.0761	-1.002	0.855
Finland vs Romania	0.684	0.0562	-4.62	< 0.001***
Finland vs UK	0.564	0.0457	-7.066	< 0.001***
Germany vs Italy	0.973	0.0805	-0.33	0.997
Germany vs Romania	0.723	0.0594	-3.945	0.000759***
Germany vs UK	0.597	0.0483	-6.377	< 0.001***
Italy vs Romania	0.743	0.0620	-3.558	0.00343**
Italy vs UK	0.613	0.0502	-5.977	< 0.001***
Romania vs UK	0.825	0.0674	-2.353	0.128

Sapele (EMMs)				
Site	**Estimated rate (mg/day)**	**SE**	**Lower 95% CI**	**Upper 95% CI**
Germany	0.626	0.0418	0.549	0.713
Italy	0.838	0.0556	0.735	0.954
Romania	0.895	0.0602	0.785	1.021
UK	1.198	0.0750	1.060	1.354
Finland	0.55	0.0385	0.479	0.631
Sapele (Tukey adjusted pairwise comparisons)				

Comparison	**Ratio**	**SE**	**z-ratio**	**p-value**
Finland vs Germany	0.879	0.0849	-1.337	0.668
Finland vs Italy	0.657	0.0632	-4.37	0.000121***
Finland vs Romania	0.614	0.0595	-5.035	< 0.001***
Finland vs UK	0.459	0.0430	-8.306	< 0.001***
Germany vs Italy	0.747	0.0702	-3.1	0.0166*
Germany vs Romania	0.699	0.0661	-3.788	0.00143**
Germany vs UK	0.522	0.0477	-7.105	1.2E-11***
Italy vs Romania	0.935	0.0882	-0.709	0.954
Italy vs UK	0.699	0.0637	-3.931	0.000805***
Romania vs UK	0.747	0.0685	-3.176	0.013*

Supplementary Table 3: Hierarchical partitioning of fixed and random effects in a GLMM of wood decomposition. Contributions are based on the lognormal conditional R^2 (0.27). Columns show the unique variance explained by each predictor, the average share of variance across predictor combinations, the individual share as the sum of unique and average shared variance, the percentage of total individual contributions, and the percentage of individual values scaled to conditional R^2.

Hierarchical partitioning of abiotic and biotic predictors

Variable	**Unique R^2**	**Average share**	**Individual**	**Individual percentage (%)**	**Percentage of conditional R^2 (%)**
Substrate	0.0671	0.002	0.0691	28.46	6.91
Site	0.0072	0.042	0.0492	20.26	4.92
Plot	NA	NA	0.025	NA	2.5
Conifer proportion	0	0.0196	0.0196	8.07	1.96
Fungi PCoA1	0.0014	0.0305	0.0319	13.14	3.19
Fungi PCoA2	0.0003	0.0065	0.0068	2.8	0.68
Soil fauna PCoA1	0.0003	0.0066	0.0069	2.84	0.69
Soil fauna PCoA2	0	0.0239	0.0239	9.84	2.39
Bacteria PCoA1	0.0005	0.005	0.0055	2.27	0.55
Bacteria PCoA2	0.0027	0.0075	0.0102	4.2	1.02
Mean temperature	0.0022	0.0111	0.0133	5.48	1.33
Mean moisture	0.0006	0.0017	0.0023	0.95	0.23
pH	0	0.0019	0.0019	0.78	0.19
Total nitrogen	-0.0002	0.0023	0.0021	0.86	0.21
Invertebrate access	-0.0002	0.0003	0.0001	0.04	0.01
Unexplained	NA	NA	NA	NA	73.22

Supplementary Table 4: Correlations between environmental predictors and soil community composition based on envfit (package vegan) analyses fitted to principal coordinates ordinations for bacteria (16S), fungi (ITS), fauna (18S; including arthropods and annelids), protists (18S), and nematodes (18S).

	Bacteria (16S)		**Fungi (ITS)**		**Fauna (18S)**		**Protist (18S)**		**Nematode (18S)**	
Predictor	**R^2**	**p-value**	**R^2**	**p-value**	**R^2**	**p-value**	**R^2**	**p-value**	**R^2**	**p-value**
pH	0.79	0.001***	0.44	0.001***	0.55	0.001***	0.76	0.001***	0.71	0.001***
Temperature	0.4	0.001***	0.88	0.001***	0.54	0.001***	0.66	0.001***	0.61	0.001***
Moisture	0.0033	0.697	0.033	0.032*	0.027	0.041*	0.035	0.017**	0.033	0.019*
Conifer proportion	0.3	0.001***	0.81	0.001***	0.58	0.001***	0.53	0.001***	0.45	0.001***
Nitrogen	0.22	0.001***	0.065	0.002**	0.38	0.001***	0.46	0.001***	0.44	0.001***
Carbon	0.18	0.001***	0.029	0.038*	0.29	0.001***	0.3	0.001***	0.28	0.001***

Supplementary Table 5: Statistical summaries of the effect of fungal (ITS2), bacterial (16S), fauna (18S; including arthropods and annelids), protist (18S), and nematode (18S) PCoA1 and PCoA2 interacting with substrate on decomposition rates with plot nested in site as a random factor. Data shows the results of generalised linear mixed effects models (GLMM), including estimates (coefficients), standard errors (SE), z-values, and p-values.

Fungal community composition				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.221	0.0618	3.575	0.00035***
Fungal PCoA1	0.19	0.0601	3.158	0.00159**
Fungal PCoA2	-0.0208	0.0593	-0.351	0.726
Pine substrate	-0.211	0.0435	-4.84	< 0.001***
Sapele substrate	-0.433	0.0438	-9.884	< 0.001***
Fungal PCoA1: Pine substrate	-0.0590	0.0459	-1.285	0.199
Fungal PCoA1: Sapele substrate	0.00305	0.0465	0.0656	0.948
Fungal PCoA2: Pine substrate	0.112	0.0396	2.839	0.00453**
Fungal PCoA2: Sapele substrate	0.0238	0.0398	0.597	0.551

Bacterial community composition				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.222	0.106	2.092	0.0364*
Bacterial PCoA1	-0.00212	0.0519	-0.041	0.967
Bacterial PCoA2	-0.0167	0.0522	0.321	0.748
Pine substrate	-0.217	0.0436	-4.97	< 0.001***
Sapele substrate	-0.444	0.0436	-10.197	< 0.001***
Bacterial PCoA1: Pine substrate	-0.0112	0.0433	-0.257	0.797
Bacterial PCoA1: Sapele substrate	0.00474	0.0438	0.108	0.914
Bacterial PCoA2: Pine substrate	0.0415	0.0415	-0.998	0.318
Bacterial PCoA2: Sapele substrate	0.00068	0.0416	-0.0163	0.987

Soil faunal community composition				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.201	0.0933	2.16	0.0308*
Faunal PCoA1	0.105	0.0594	1.766	0.0775
Faunal PCoA2	-0.0196	0.0737	-0.266	0.79
Pine substrate	-0.195	0.0447	-4.366	0.0000127***
Sapele substrate	-0.421	0.0449	-9.376	< 0.001***
Faunal PCoA1: Pine substrate	-0.072	0.0490	-1.471	0.141
Faunal PCoA1: Sapele substrate	-0.0408	0.0498	-0.82	0.412
Faunal PCoA2: Pine substrate	0.0219	0.0399	0.55	0.582
Faunal PCoA2: Sapele substrate	0.0291	0.0394	0.74	0.459

Protist community composition				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.212	0.0676	3.141	0.00168**
Protist PCoA1	0.0734	0.0681	1.078	0.281
Protist PCoA2	0.164	0.0733	-2.23	0.0258*
Pine substrate	-0.189	0.0477	-3.956	0.0000762***
Sapele substrate	-0.415	0.048	-8.651	< 0.001***
Protist PCoA1: Pine substrate	-0.0478	0.0509	-0.941	0.347
Protist PCoA1: Sapele substrate	-0.019	0.0515	-0.369	0.712
Protist PCoA2: Pine substrate	-0.0627	0.0563	1.113	0.266
Protist PCoA2: Sapele substrate	-0.00881	0.0562	0.157	0.875

Nematode community composition				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.206	0.0697	2.947	0.00321**
Nematode PCoA1	0.134	0.06	2.234	0.0255*
Nematode PCoA2	0.129	0.0686	1.876	0.0607
Pine substrate	-0.188	0.0478	-3.934	0.0000837***

Sapele substrate	-0.412	0.0481	-8.577	< 0.001***
Nematode PCoA1: Pine substrate	-0.0682	0.0538	-1.267	0.205
Nematode PCoA1: Sapele substrate	-0.0483	0.054	-0.895	0.371
Nematode PCoA2: Pine substrate	-0.0559	0.0558	-1.001	0.317
Nematode PCoA2: Sapele substrate	-0.0153	0.0557	-0.274	0.784

Supplementary Table 6: Post-hoc marginal effects average slope test showing estimated changes in decomposition rate (mg/day^{-1}) for every one unit increase in fungal (ITS2), bacterial (16S), faunal (18S; including arthropods and annelids), protist (18S), and nematode (18S) PCoA1 or PCoA2 per substrate. Results extracted from a GLMM, including estimates (coefficients), standard errors (SE), z-values, p-values, the lower confidence interval, and upper confidence interval.

Fungal PCoA1						
Substrate	**Estimate**	**SE**	**z-value**	**p-value**	**Lower 95% CI**	**Upper 95% CI**
Birch	0.237	0.0801	2.959	0.00309**	0.08	0.394
Pine	0.124	0.0534	2.325	0.0201*	0.0195	0.229
Sapele	0.147	0.0447	3.285	0.00102**	0.0593	0.235
Fungal PCoA2						
Substrate	**Estimate**	**SE**	**z-value**	**p-value**	**Lower 95% CI**	**Upper 95% CI**
Birch	-0.026	0.0741	-0.351	0.726	-0.171	0.119
Pine	0.087	0.0578	1.505	0.132	-0.0263	0.2
Sapele	0.00225	0.0458	0.0491	0.961	-0.0875	0.0920

Bacterial PCoA1						
Substrate	**Estimate**	**SE**	**z-value**	**p-value**	**Lower 95% CI**	**Upper 95% CI**
Birch	-0.00266	0.065	-0.0409	0.967	-0.13	0.125
Pine	-0.0125	0.0473	-0.265	0.791	-0.105	0.0801
Sapele	0.00188	0.0379	0.0495	0.96	-0.072	0.0761
Bacterial PCoA2						
Substrate	**Estimate**	**SE**	**z-value**	**p-value**	**Lower 95% CI**	**Upper 95% CI**
Birch	0.0206	0.0654	0.315	0.753	-0.149	0.1076

Pine	-0.024	0.0487	-0.492	0.622	-0.0714	0.1193
Sapele	0.012	0.0388	0.308	0.758	-0.0881	0.0641

Faunal PCoA1						
Substrate	**Estimate**	**SE**	**z-value**	**p-value**	**Lower 95% CI**	**Upper 95% CI**
Birch	0.131	0.0775	1.689	0.0913	-0.021	0.283
Pine	0.0313	0.0529	0.591	0.554	-0.0724	0.135
Sapele	0.0489	0.0444	1.102	0.271	-0.0381	0.136
Faunal PCoA2						
Substrate	**Estimate**	**SE**	**z-value**	**p-value**	**Lower 95% CI**	**Upper 95% CI**
Birch	-0.0245	0.0915	-0.267	0.789	-0.204	0.155
Pine	0.00222	0.0691	0.0321	0.974	-0.133	0.138
Sapele	0.00727	0.0564	0.129	0.897	-0.103	0.118

Protist PCoA1						
Substrate	**Estimate**	**SE**	**z-value**	**p-value**	**Lower 95% CI**	**Upper 95% CI**
Birch	0.0916	0.087	1.053	0.292	-0.0789	0.262
Pine	0.0243	0.0559	0.434	0.664	-0.0854	0.134
Sapele	0.0415	0.0455	0.912	0.362	-0.0477	0.131
Protist PCoA2						
Substrate	**Estimate**	**SE**	**z-value**	**p-value**	**Lower 95% CI**	**Upper 95% CI**
Birch	-0.204	0.0976	-2.091	0.0365*	0.0128	0.395
Pine	-0.0959	0.0566	-1.695	0.0901	-0.0150	0.207

Sapele	-0.118	0.0473	-2.495	0.0126*	0.0253	0.211

Nematode PCoA1						
Substrate	**Estimate**	**SE**	**z-value**	**p-value**	**Lower 95% CI**	**Upper 95% CI**
Birch	0.167	0.0778	2.151	0.0315*	0.0149	0.32
Pine	0.0625	0.0463	1.348	0.178	-0.0283	0.153
Sapele	0.0654	0.0373	1.753	0.0796	-0.00772	0.138
Nematode PCoA2						
Substrate	**Estimate**	**SE**	**z-value**	**p-value**	**Lower 95% CI**	**Upper 95% CI**
Birch	0.161	0.0898	1.791	0.0732	-0.0151	0.337
Pine	0.0691	0.0529	1.306	0.192	-0.0346	0.173
Sapele	0.0865	0.044	1.967	0.0492*	0.000321	0.173

Supplementary Table 7: Statistical summaries of the effect of wood saprotrophic, total saprotrophic (including those capable of decomposing wood, litter and soil), and ectomycorrhizal (EcM) fungal (ITS2) PCoA1 and PCoA2 interacting with substrate on decomposition rates (mg/day^{-1}) with plot nested in site as a random factor. Data shows the results of generalised linear mixed effects models (GLMM), including estimates (coefficients), standard errors (SE), z-values, and p-values.

Wood saprotrophic community composition				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.23	0.0436	5.272	< 0.001***
Wood saprotroph PCoA1	0.209	0.0446	4.68	< 0.001***
Wood saprotroph PCoA2	0.0120	0.0392	0.307	0.759
Pine substrate	-0.217	0.043	-5.041	< 0.001***
Sapele substrate	-0.44	0.0433	-10.145	< 0.001***
Wood saprotroph PCoA1: Pine substrate	-0.0457	0.0444	-1.028	0.304
Wood saprotroph PCoA1: Sapele substrate	0.0203	0.0448	0.453	0.650
Wood saprotroph PCoA2: Pine substrate	-0.114	0.0398	-2.871	0.00409**
Wood saprotroph PCoA2: Sapele substrate	-0.0222	0.0399	-0.557	0.578

Total saprotrophic community composition				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.222	0.0488	4.545	< 0.001***
Total saprotroph PCoA1	0.213	0.0495	4.308	< 0.001***
Total saprotroph PCoA2	0.0778	0.0465	1.673	0.0944
Pine substrate	-0.208	0.0436	-4.766	< 0.001***
Sapele substrate	-0.43	0.0439	-9.787	< 0.001***
Total saprotroph PCoA1: Pine substrate	-0.103	0.0459	-2.252	0.0243*

Total saprotroph PCoA1: Sapele substrate	-0.00927	0.0461	-0.201	0.841
Total saprotroph PCoA2: Pine substrate	0.0811	0.0409	1.983	0.0474*
Total saprotroph PCoA2: Sapele substrate	0.0272	0.0412	0.659	0.510

EcM community composition				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.191	0.0825	2.321	0.0203*
EcM PCoA1	-0.0894	0.0898	-0.996	0.319
EcM PCoA2	-0.108	0.0569	-1.893	0.0583
Pine substrate	-0.192	0.0448	-4.284	0.0000183***
Sapele substrate	-0.408	0.0453	-9.005	< 0.001***
EcM PCoA1: Pine substrate	0.0091	0.0451	0.202	0.84
EcM PCoA1: Sapele substrate	0.0216	0.0460	0.470	0.638
EcM PCoA2: Pine substrate	0.169	0.0485	3.486	0.00049***
EcM PCoA2: Sapele substrate	0.0464	0.0482	0.962	0.336

Supplementary Table 8: Post-hoc marginal effects average slope test showing estimated changes in decomposition rate (mg/day^{-1}) for every one unit increase in wood saprotrophic, total saprotrophic (including those capable of decomposing wood, litter and soil), or ectomycorrhizal (EcM) fungal (ITS2) PCoA1 and PCoA2 per substrate. Results extracted from a GLMM, including estimates (coefficients), standard errors (SE), z-values, p-values, the lower confidence interval, and upper confidence interval.

Wood saprotroph PCoA1						
Substrate	**Estimate**	**SE**	**z-value**	**p-value**	**Lower 95% CI**	**Upper 95% CI**
Birch	0.261	0.0593	4.413	0.0000102***	0.145	0.378
Pine	0.155	0.0385	4.025	0.0000569***	0.0795	0.23
Sapele	0.175	0.0325	5.383	< 0.001***	0.111	0.239
Wood saprotroph PCoA2						
Substrate	**Estimate**	**SE**	**z-value**	**p-value**	**Lower 95% CI**	**Upper 95% CI**
Birch	0.015	0.049	0.307	0.759	-0.0811	0.111
Pine	-0.0971	0.0385	-2.525	0.012*	-0.172	-0.0217
Sapele	-0.00779	0.0307	-0.254	0.799	-0.0679	0.0523

Total saprotroph PCoA1						
Substrate	**Estimate**	**SE**	**z-value**	**p-value**	**Lower 95% CI**	**Upper 95% CI**
Birch	0.266	0.0658	4.053	0.0000507***	0.138	0.395
Pine	0.104	0.0413	2.528	0.0115*	0.0234	0.185
Sapele	0.156	0.0350	4.443	< 0.001***	0.0870	0.224
Total saprotroph PCoA2						
Substrate	**Estimate**	**SE**	**z-value**	**p-value**	**Lower 95% CI**	**Upper 95% CI**

Birch	0.0972	0.0587	1.654	0.0981	-0.018	0.212
Pine	0.151	0.0448	3.369	0.000754***	0.0631	0.239
Sapele	0.0801	0.0356	2.247	0.0246*	0.0102	0.15

EcM PCoA1						
Substrate	**Estimate**	**SE**	**z-value**	**p-value**	**Lower 95% CI**	**Upper 95% CI**
Birch	-0.112	0.116	-0.962	0.336	-0.340	0.116
Pine	-0.0761	0.0862	-0.883	0.377	-0.245	0.0928
Sapele	-0.0517	0.0701	-0.739	0.460	-0.189	0.0856
EcM PCoA2						
Substrate	**Estimate**	**SE**	**z-value**	**p-value**	**Lower 95% CI**	**Upper 95% CI**
Birch	-0.135	0.0754	-1.791	0.0733	-0.283	0.0128
Pine	0.0581	0.0517	1.123	0.262	-0.0433	0.159
Sapele	-0.0469	0.0425	-1.103	0.270	-0.13	0.0364

Supplementary Table 9: Statistical summaries of the effect of fungal (ITS2), bacterial (16S), fauna (18S; including arthropods and annelids), protist (18S), and nematode (18S) richness, Simpson or Shannon diversity interacting with substrate on decomposition rates with plot nested in site as a random factor. Data shows the results of generalised linear mixed effects models (GLMM), including estimates (coefficients), standard errors (SE), z-values, and p-values.

Fungal richness				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.22	0.1	2.09	0.037*
Fungal richness	0.020	0.033	0.6	0.55
Pine substrate	-0.21	0.043	-4.99	<0.001***
Sapele substrate	-0.44	0.043	-10.39	<0.001***
Fungal richness: Pine substrate	-0.01	0.041	-0.16	0.87
Fungal richness: Sapele substrate	-0.034	0.04	-0.84	0.4

Fungal Simpson diversity				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.22	0.11	2.02	0.044*
Fungal Simpson	0.019	0.031	0.61	0.54
Pine substrate	-0.21	0.043	-4.96	<0.001***
Sapele substrate	-0.44	0.043	-10.3	<0.001***
Fungal Simpson: Pine substrate	-0.064	0.04	-1.61	0.11
Fungal Simpson: Sapele substrate	-0.032	0.042	-0.76	0.45

Fungal Shannon diversity				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.22	0.11	2.02	0.044*
Fungal Shannon	0.012	0.033	0.36	0.72
Pine substrate	-0.21	0.043	-4.95	<0.001***
Sapele substrate	-0.44	0.043	-10.28	<0.001***

Fungal Shannon: Pine substrate	-0.044	0.041	-1.08	0.28
Fungal Shannon: Sapele substrate	-0.016	0.042	-0.39	0.69

Bacterial richness				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.21	0.10	2.1	0.035*
Bacterial richness	0.0	0.0	1.25	0.21
Pine substrate	-0.21	0.043	-4.81	<0.001***
Sapele substrate	-0.44	0.043	-10.11	<0.001***
Bacterial richness: Pine substrate	0.0	0.043	-0.69	0.49
Bacterial richness: Sapele substrate	-0.026	0.044	-0.6	0.55

Bacterial Simpson diversity				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.23	0.1	2.3	0.022*
Bacterial Simpson	0.012	0.038	0.31	0.76
Pine substrate	-0.22	0.043	-5.08	<0.001***
Sapele substrate	-0.45	0.043	-10.45	<0.001***
Bacterial Simpson: Pine substrate	0.039	0.041	0.94	0.35
Bacterial Simpson: Sapele substrate	0.024	0.041	0.58	0.56

Bacterial Shannon diversity				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.22	0.1	2.14	0.033*
Bacterial Shannon	0.025	0.042	0.61	0.54
Pine substrate	-0.21	0.043	-4.92	<0.001***
Sapele substrate	-0.44	0.043	-10.25	<0.001***
Bacterial Shannon: Pine substrate	-0.012	0.042	-0.28	0.78

Bacterial Shannon: Sapele substrate	-0.011	0.043	-0.26	0.8

Protist richness				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.21	0.11	1.92	0.055
Protist richness	-0.00033	0.036	-0.0091	0.99
Pine substrate	-0.2	0.043	-4.74	<0.001***
Sapele substrate	-0.43	0.043	-10.07	<0.001***
Protist richness: Pine substrate	-0.048	0.041	-1.17	0.24
Protist richness: Sapele substrate	-0.017	0.042	-0.41	0.68

Protist Simpson diversity				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.21	0.11	2.01	0.04*
Protist Simpson	0.017	0.034	0.49	0.62
Pine substrate	-0.2	0.043	-4.74	<0.001***
Sapele substrate	-0.43	0.043	-10.1	<0.001***
Protist Simpson: Pine substrate	-0.030	0.041	-0.74	0.46
Protist Simpson: Sapele substrate	-0.019	0.041	-0.47	0.64

Protist Shannon diversity				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.21	0.11	1.93	0.054
Protist Shannon	0.015	0.036	0.41	0.68
Pine substrate	-0.2	0.043	-4.72	<0.001***
Sapele substrate	-0.43	0.043	-10.04	<0.001***
Protist Shannon: Pine substrate	-0.059	0.042	-1.39	0.16
Protist Shannon: Sapele substrate	-0.029	0.043	-0.69	0.49

Faunal richness				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.22	0.1	2.16	0.03*
Faunal richness	-0.064	0.033	-1.94	0.053
Pine substrate	-0.22	0.043	-5.12	<0.001***
Sapele substrate	-0.45	0.043	-10.42	<0.001***
Faunal richness: Pine substrate	0.088	0.042	2.079	0.038
Faunal richness: Sapele substrate	0.11	0.043	2.58	0.01

Faunal Simpson diversity				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.24	0.10	2.27	0.023*
Faunal Simpson	-0.047	0.03	-1.56	0.12
Pine substrate	-0.23	0.043	-5.31	<0.001***
Sapele substrate	-0.45	0.043	-10.41	<0.001***
Faunal Simpson: Pine substrate	0.07	0.041	1.71	0.088
Faunal Simpson: Sapele substrate	0.047	0.042	1.12	0.26

Faunal Shannon diversity				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.22	0.10	2.14	0.032
Faunal Shannon	-0.063	0.033	-1.89	0.059
Pine substrate	-0.22	0.043	-5.09	<0.001***
Sapele substrate	-0.45	0.043	-10.38	<0.001***
Faunal Shannon: Pine substrate	0.085	0.042	2.02	0.043
Faunal Shannon: Sapele substrate	0.093	0.043	2.17	0.03

Nematode richness				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.23	0.1	2.23	0.026*
Nematode richness	0.035	0.032	1.07	0.28
Pine substrate	-0.23	0.043	-5.23	<0.001***
Sapele substrate	-0.45	0.043	-10.36	<0.001***
Nematode richness: Pine substrate	-0.026	0.042	-0.62	0.54
Nematode richness: Sapele substrate	-0.054	0.042	-1.29	0.2

Nematode Simpson diversity				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.22	0.11	2.07	0.038*
Nematode Simpson	0.046	0.034	1.37	0.17
Pine substrate	-0.21	0.043	-4.98	<0.001***
Sapele substrate	-0.44	0.043	-10.32	<0.001***
Nematode Simpson: Pine substrate	-0.041	0.042	-0.97	0.33
Nematode Simpson: Sapele substrate	-0.066	0.042	-1.57	0.12

Nematode Shannon diversity				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.22	0.10	2.09	0.037*
Nematode Shannon	0.042	0.031	1.34	0.18
Pine substrate	-0.21	0.043	-4.98	<0.001***
Sapele substrate	-0.44	0.043	-10.33	<0.001***
Nematode Shannon: Pine substrate	-0.034	0.04	-0.86	0.39
Nematode Shannon: Sapele substrate	-0.075	0.04	-1.88	0.06

Supplementary Table 10: Statistical summaries of the effect of wood saprotrophic, total saprotrophic (including those capable of decomposing wood, litter and soil), and ectomycorrhizal (EcM) fungal (ITS2) richness, Simpson or Shannon diversity interacting with substrate on decomposition rates (mg/day^{-1}) with plot nested in site as a random factor. Data shows the results of generalised linear mixed effects models (GLMM), including estimates (coefficients), standard errors (SE), z-values, and p-values.

Wood saprotroph richness				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.23	0.1	2.27	0.023*
Wood saprotroph richness	-0.022	0.036	-0.61	0.54
Pine substrate	-0.22	0.043	-5.15	<0.001***
Sapele substrate	-0.45	0.043	-10.48	<0.001***
Wood saprotroph richness: Pine substrate	0.05	0.043	1.16	0.24
Wood saprotroph richness: Sapele substrate	0.046	0.042	1.1	0.27

Wood saprotroph Simpson diversity				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.22	0.11	2.02	0.044*
Wood saprotroph Simpson	-0.022	0.034	-0.65	0.51
Pine substrate	-0.21	0.043	-5.01	<0.001***
Sapele substrate	-0.44	0.043	-10.39	<0.001***
Wood saprotroph Simpson: Pine substrate	0.017	0.042	0.4	0.69
Wood saprotroph Simpson: Sapele substrate	-0.029	0.042	-0.69	0.49

Wood saprotroph Shannon diversity				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**

(Intercept)	0.22	0.11	2.02	0.043*
Wood saprotroph Shannon	-0.0049	0.037	-0.13	0.89
Pine substrate	-0.21	0.043	-4.97	<0.001***
Sapele substrate	-0.44	0.043	-10.34	<0.001***
Wood saprotroph Shannon: Pine substrate	-0.01	0.044	-0.22	0.82
Wood saprotroph Shannon: Sapele substrate	-0.026	0.045	-0.58	0.57

Total saprotroph richness				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.22	0.1	2.07	0.039
Total saprotroph richness	0.036	0.033	1.1	0.27
Pine substrate	-0.21	0.043	-4.96	<0.001***
Sapele substrate	-0.44	0.043	-10.33	<0.001***
Total saprotroph richness: Pine substrate	-0.038	0.041	-0.93	0.35
Total saprotroph richness: Sapele substrate	-0.030	0.040	-0.76	0.45

Total saprotroph Simpson diversity				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.22	0.10	2.09	0.037*
Total saprotroph Simpson	0.013	0.032	0.39	0.69
Pine substrate	-0.21	0.043	-5.02	<0.001***
Sapele substrate	-0.44	0.043	-10.39	<0.001***
Total saprotroph Simpson: Pine substrate	-0.038	0.04	-0.95	0.34

Total saprotroph Simpson: Sapele substrate	-0.0053	0.042	-0.13	0.9

Total saprotroph Shannon diversity				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.22	0.1	2.10	0.036*
Total saprotroph Shannon	0.029	0.033	0.87	0.38
Pine substrate	-0.21	0.043	-5.00	<0.001***
Sapele substrate	-0.44	0.042	-10.41	<0.001***
Total saprotroph Shannon: Pine substrate	-0.048	0.041	-1.18	0.24
Total saprotroph Shannon: Sapele substrate	0.01	0.042	0.23	0.82

EcM richness				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.22	0.10	2.11	0.035*
EcM richness	0.006	0.036	0.17	0.87
Pine substrate	-0.22	0.043	-5.06	<0.001***
Sapele substrate	-0.44	0.043	-10.40	<0.001***
EcM richness: Pine substrate	0.025	0.042	0.60	0.55
EcM richness: Sapele substrate	-0.042	0.042	-1.00	0.32

EcM Simpson diversity				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.24	0.10	2.28	0.023*
EcM Simpson	-0.0018	0.029	-0.06	0.95
Pine substrate	-0.23	0.043	-5.31	<0.001***

Sapele substrate	-0.45	0.043	-10.51	<0.001***
EcM Simpson: Pine substrate	0.019	0.040	0.48	0.63
EcM Simpson: Sapele substrate	-0.016	0.041	-0.38	0.7

EcM Shannon diversity				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.22	0.11	2.09	0.037*
EcM Shannon	0.013	0.031	0.43	0.67
Pine substrate	-0.21	0.043	-5.04	<0.001***
Sapele substrate	-0.44	0.042	-10.43	<0.001***
EcM Shannon: Pine substrate	0.029	0.041	0.7	0.48
EcM Shannon: Sapele substrate	-0.018	0.041	-0.45	0.65

Supplementary Table 11: Statistical summaries of the effect of each microclimate metric on decomposition including temperature, soil moisture and soil suitability index. Temperature and moisture models included a quadratic (nonlinear) term and the soil suitability model included a single linear term. All models had an interaction with substrate and plot nested in site as a random factor. Data shows the results of generalised linear mixed effects models (GLMM), including estimates (coefficients), standard errors (SE), z-values, and p-values.

Temperature				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.296	0.136	2.182	0.0291
Pine substrate	-0.198	0.066	-2.989	0.0028**
Sapele substrate	-0.402	0.067	-6.012	< 0.001***
Mean daily microclimate temperature	0.172	0.100	1.719	0.0855
Mean daily microclimate temperature ^2	-0.0953	0.115	-0.827	0.408
Pine substrate: Mean daily microclimate temperature	-0.130	0.0666	-1.959	0.0501
Sapele substrate: Mean daily microclimate temperature	-0.0183	0.0666	-0.275	0.783
Pine substrate: Mean daily microclimate temperature ^2	0.00462	0.0728	0.0635	0.949
Sapele substrate: Mean daily microclimate temperature ^2	0.00027	0.0729	0.0037	0.997

Soil moisture				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.281	0.114	2.468	0.0136*
Pine substrate	-0.281	0.0493	-5.705	<0.001***
Sapele substrate	-0.499	0.0496	-10.064	<0.001***
Mean daily soil moisture	-0.104	0.036	-2.88	0.00398**
Mean daily soil moisture ^2	-0.124	0.0293	-4.233	<0.001***

Pine substrate: Mean daily soil moisture	0.134	0.046	2.905	0.00368**
Sapele substrate: Mean daily soil moisture	0.0786	0.0477	1.648	0.0993
Pine substrate: Mean daily soil moisture ^2	0.124	0.0322	3.85	0.000118**
Sapele substrate: Mean daily soil moisture ^2	0.126	0.0329	3.822	0.000133**

Soil suitability index				
Parametric terms	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.203	0.113	1.793	0.073
Mean daily soil suitable index	0.0283	0.0325	0.87	0.384
Pine substrate	-0.203	0.0421	-4.816	<0.001***
Sapele substrate	-0.421	0.0420	-10.027	<0.001***
Pine substrate: Mean daily soil suitable index	-0.0544	0.0414	-1.314	0.189
Sapele substrate: Mean daily soil suitable index	-0.0166	0.0429	-0.386	0.7

Supplementary Table 12: Post-hoc marginal effects average slope test showing estimated changes in decomposition rate (mg/day^{-1}) for every one unit increase in mean microclimate temperature, soil moisture, and soil suitability index per substrate. Results extracted from a GLMM, including estimates (coefficients), standard errors (SE), z-values, p-values, the lower confidence interval, and upper confidence interval.

Temperature						
Substrate	**Estimate**	**SE**	**z-value**	**p-value**	**Lower 95% CI**	**Upper 95% CI**
Birch	0.134	0.0973	1.376	0.169	-0.0568	0.324
Pine	0.0438	0.0674	0.649	0.516	-0.0883	0.176
Sapele	0.104	0.0516	2.008	0.0446*	0.00248	0.205

Soil moisture						
Substrate	**Estimate**	**SE**	**z-value**	**p-value**	**Lower 95% CI**	**Upper 95% CI**
Birch	-0.0582	0.0446	-1.303	0.192	-0.146	0.0293
Pine	0.0278	0.0303	0.917	0.359	-0.0316	0.0872
Sapele	-0.0191	0.0274	-0.697	0.486	-0.0729	0.0346

Soil suitability index						
Substrate	**Estimate**	**SE**	**z-value**	**p-value**	**Lower 95% CI**	**Upper 95% CI**
Birch	0.035	0.0405	0.865	0.387	-0.0443	0.114
Pine	-0.0243	0.0269	-0.904	0.366	-0.077	0.0284
Sapele	0.00883	0.0231	0.383	0.702	-0.0363	0.054

Supplementary Table 13: Statistical summaries of the association between soil nitrogen and soil pH on decomposition rate (mg/day^{-1}). Each term had an interaction with substrate and plot nested in site as a random factor. Data shows the results of generalised linear mixed effects models (GLMM), including estimates (coefficients), standard errors (SE), z-values, and p-values.

Soil nutrients and pH				
Substrate	**Estimate**	**SE**	**z-value**	**p-value**
(Intercept)	0.202	0.11	0.865	0.387
Total nitrogen	0.0302	0.0382	-0.904	0.366
pH	-0.018	0.0404	0.383	0.702
Pine substrate	-0.210	0.0402	1.836	0.0663
Sapele substrate	-0.433	0.0402	0.789	0.43
Total nitrogen: Pine substrate	-0.0525	0.0413	-0.446	0.656
Total nitrogen: Sapele substrate	0.00314	0.0418	-5.209	<0.001***
pH: Pine substrate	-0.00448	0.0419	-10.781	<0.001***
pH: Sapele substrate	0.0252	0.0433	-1.271	0.204

Supplementary Table 14: The location of the five focal study sites, forest type, dominant tree species, the mean annual temperature and precipitation (summarised from the years 2022 and 2023 from the ERA5 database), the dates wood sticks were installed and removed, and the number of days on the ground.

Site location	**Forest type**	**Dominant tree species**	**Annual temperature and precipitation**	**Date of wood stick placement**	**Date of wood stick removal**	**Days on the ground**
Râșca, Romania 47.28891, 26.05292	Montane temperate	*Abies alba*, *Picea abies* and *Fagus sylvatica*	7.7°C 8,532 mm	24th October 2021	19th October 2023	725
Tatti Forest, Italy 43.34561, 10.960644	Mediterranean thermophilous	*Quercus petraea*, *Quercus ilex* and *Quercus cerris*	15.3°C 11,134 mm	10th November 2021	23rd October 2023	712
Mathislewald, Germany 47.88651, 8.08588	Montane temperate	*Picea abies*	8.9°C 17,212 mm	26th November 2021	25th November 2023	729
Ausewell Woods, UK 50.52178, -3.79850	Temperate rainforest	*Quercus petraea* and *Ilex aquifolium*	12°C 11,126 mm	4th December 2021	8th December 2023	734
Savonranta, Finland 62.26743, 28.94798	Boreal	*Picea abies*, *Betula pendula* and *Betula pubescens*	4.7°C 11,026 mm	13th June 2022	6th July 2024	754

Supplementary Table 15: Eigenvalues for principal coordinate analysis axes one and two for soil biotic groups considered in the study.

Group	Axis	Eigenvalue
Fungi (ITS)	PCoA1	11.7
Fungi (ITS)	PCoA2	10.9
Bacteria (16S)	PCoA1	20.8
Bacteria (16S)	PCoA2	7.2
Protists (18S)	PCoA1	12.5
Protists (18S)	PCoA2	6.8
Fauna (18S)	PCoA1	6.3
Fauna (18S)	PCoA2	5.1
Nematodes (18S)	PCoA1	10.9
Nematodes (18S)	PCoA2	6.3
Wood saprotrophic fungi (ITS)	PCoA1	11.7
Wood saprotrophic fungi (ITS)	PCoA2	10.7
Saprotrophic fungi (ITS)	PCoA1	12.9
Saprotrophic fungi (ITS)	PCoA2	12.6
Ectomycorrhizal fungi (ITS)	PCoA1	9.6
Ectomycorrhizal fungi (ITS)	PCoA2	5.8

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